Listing of the Claims

This listing of claims will replace all prior versions, and listings of claims in the application.

1. (Previously presented) A method of identifying, analyzing or typing a polymorphic DNA fragment in a sample of DNA, said method comprising: (a) contacting said sample of DNA with one or more DNA polymerases, wherein said one or more DNA polymerases comprise one or more mutations or modifications in the O-helix of said one or more DNA polymerases which reduce their ability to add one or more non-templated nucleotides to the 3′ terminus of a synthesized DNA molecule; (b) amplifying said polymorphic DNA fragment within said sample to produce a population of amplified DNA fragments, wherein less than about 50% of said amplified DNA fragments have one or more non-templated 3′ nucleotides compared to amplification products produced by *Taq* DNA polymerase assayed under the same conditions; and (c) analyzing said amplified polymorphic DNA fragment.

2. (Previously presented) A method of producing amplified copies of a polymorphic DNA fragment, said method comprising: a) contacting a DNA sample with one or more DNA polymerases, wherein said one or more DNA polymerases comprise one or more mutations or modifications in the O-helix of said one or more DNA polymerases which reduce their ability to add one or more non-templated nucleotides to the 3′ terminus of a synthesized DNA

molecule; and b) amplifying said polymorphic DNA fragment within said DNA sample to produce a population of amplified DNA fragments, wherein less than about 50% of said amplified DNA fragments have one or more non-templated 3′ nucleotides compared to amplification products produced by *Taq* DNA polymerase assayed under the same conditions.

3-4. (Canceled)

5. (Original) The method of claim 1, wherein said polymorphic DNA fragment is selected from the group of polymorphic DNA fragments comprising a minisatellite DNA fragment, a microsatellite DNA fragment and a STR DNA fragment.

6. (Original) The method of claim 1, wherein said polymerases are thermostable DNA polymerases.

7. (Previously presented) The method of claim 6, wherein the thermostable DNA polymerases are *Thermotoga* DNA polymerases or mutants thereof.

8. (Original) The method of claim 7, wherein said DNA polymerase is a *Tne* or *Tma* DNA polymerase.

9. (Previously presented) The method of claim 1, wherein said DNA polymerases are reduced in 3′-5′ exonuclease activity.

10. (Previously presented) The method of claim 1, wherein said DNA polymerases are reduced in 5′-3′ exonuclease activity.

11. (Previously presented) The method of claim 9, wherein said DNA polymerases are reduced in 5′-3′ exonuclease activity.

12. (Canceled)

13. (Previously presented) The method of claim 1, wherein said DNA polymerases are reduced in at least one activity selected from the group consisting of:

    (a) 3′-5′ exonuclease activity; and

    (b) 5′-3′ exonuclease activity.

14. (Previously presented) The method of claim 13, wherein said polymerases have reduced 3′-5′ exonuclease and 5′-3′ exonuclease activity.

15. (Previously presented) The method of claim 13, wherein said polymerase is reduced in 3′-5′ exonuclease activity.

16. (Canceled)

17. (Previously presented) The method of claim 1, wherein said O-helix is defined as RXXXKXXXFXXXYX (SEQ ID NO: 11), wherein X is any amino acid.

18. (Original) The method of claim 17, wherein said mutation or modification is at position R (Arg) and/or F (Phe) and/or K (Lys) of said O-helix or combinations thereof.

19. (Original) The method of claim 1, wherein said polymerase is selected from the group consisting of: *Tne* N′Δ219, D323A; *Tne* N′Δ283, D323A; *Tne* N′Δ284, D323A; *Tne* N′Δ193, D323A; *Tne* D137A, D323A; *Tne* D8A, D323A; *Tne* G195D, D323A; *Tne* G37D, D323A; *Tne* N'Δ283; *Tne* D137A, D323A, R722K; *Tne* D137A, D323A, R722Y; *Tne* D137A, D323A, R722L; *Tne* D137A, D323A, R722H; *Tne* D137A, D323A, R722Q; *Tne* D137A, D323A, F730Y; *Tne* D137A, D323A, K726R; *Tne* D137A, D323A, K726H; *Tne* D137A, D323A, R722K, F730Y; *Tne* D137A, D323A, R722K, K726R; *Tne* D137A, D323A, R722K, K726H; *Tne* D137A, D323A, R722H, F730Y; *Tne* D137A, D323A, R722H, K726R; *Tne* D137A, D323A, R722H, K726H; *Tne* D137A, D323A, R722Q, F730Y; *Tne* D137A, D323A, R722Q, K726R; *Tne* D137A, D323A, R722N, F730Y; *Tne* D137A, D323A, R722N, K726R; *Tne* D137A, D323A, R722N, K726H; *Tne* D137A, D323A, F730S; *Tne* N'Δ283, D323A, R722K/H/Q/N/Y/L; *Tne* N′Δ219, D323A, R722K; *Tne* N′Δ219, D323A, F730Y; *Tne* N′Δ219, D323A, K726R; *Tne* N′Δ219, D323A, K726H; *Tne* D137A, D323A, F730S, R722K/Y/Q/N/H/L, K726R/H; *Tne* D137A, D323A, F730T, R722K/Y/Q/N/H/L, K726R/H; *Tne* D137A, D323A, F730T; *Tne* F730S; *Tne* F730A; *Tne* K726R; *Tne* K726H; and *Tne* D137A, D323A, R722N.

20. (Previously presented) The method of claim 1, wherein said mutation or modification is an amino acid substitution at position R and/or F and/or K of said O-helix or combinations thereof.

21. (Previously presented) A method of determining the relationship between a first individual and a second individual, said method comprising comparing a population of amplified DNA molecules in a sample of DNA from said first individual to that of said second individual, wherein said DNA sample of said first and second individuals are analyzed according to the method of claim 1.

22. (Original) The method of claim 21, wherein said sample of DNA from said first individual is a known sample and said sample of DNA from said second individual is an unknown sample.

23. (Previously presented) A kit comprising one or more DNA polymerases, wherein said one or more DNA polymerases comprise one or more mutations or modifications in the O-helix of said one or more DNA polymerases which reduce their ability to add one or more non-templated nucleotides to the 3' terminus of a synthesized DNA molecule, and wherein amplification of a polymorphic DNA fragment with said DNA polymerase produces a population of DNA fragments in which less than about 50% of said DNA fragments have one or more non-templated 3' nucleotides compared to amplification products produced by *Taq* DNA polymerase assayed under the same conditions.

24. (Original) The kit of claim 23, said kit further comprising one or more components selected from the group consisting of one or more DNA primers,

one or more deoxynucleoside triphosphates, and a buffer suitable for use in the identification, analysis or typing of a polymorphic DNA fragment.

25. (Original) The kit of claim 23, wherein said polymerases are thermostable DNA polymerases.

26. (Previously presented) The kit of claim 25, wherein said thermostable DNA polymerases are *Thermotoga* DNA polymerases.

27. (Previously presented) The kit of claim 23, wherein said DNA polymerase is reduced in 3′-5′ exonuclease activity.

28. (Previously presented) The kit of claim 23, wherein said DNA polymerase is reduced in 5′-3′ exonuclease activity.

29. (Canceled).

30. (Canceled).

31. (Previously presented) The kit of claim 23, wherein said O-helix is defined as RXXXKXXXFXXXYX (SEQ ID NO: 11), wherein X is any amino acid.

32. (Original) The kit of claim 31, wherein said mutation or modification is at position R (Arg) and/or F (Phe) and/or K (Lys) of said O-helix or combinations thereof.

33. (Previously presented) The kit of claim 31, wherein said mutation or modification is an amino acid substitution at position R and/or F and/or K of said O-helix or combinations thereof.

34-65. (Canceled)

66. (Previously presented) A method for amplifying a double stranded DNA molecule, comprising:

(a) providing a first and second primer, wherein said first primer is complementary to a sequence at or near the 3′-terminus of the first strand of said DNA molecule and said second primer is complementary to a sequence at or near the 3′-terminus of the second strand of said DNA molecule;

(b) hybridizing said first primer to said first strand and said second primer to said second strand in the presence of one or more DNA polymerases, wherein said one or more DNA polymerases comprise one or more mutations or modifications in the O-helix of said one or more DNA polymerases which reduce their ability to add non-templated 3′ nucleotides to a synthesized nucleic acid molecule under conditions such that a third DNA molecule complementary to said first strand and a fourth DNA molecule complementary to said second strand are synthesized;

(c) denaturing said first and third strands, and said second and fourth strands; and

(d) repeating steps (a) to (c) one or more times to produce a population of amplified DNA fragments, wherein less than about 50% of said amplified DNA fragments have one or more non-templated 3′ nucleotides compared to amplification products produced by *Taq* DNA polymerase assayed under the same conditions.

67-68. (Canceled).

69. (Previously presented) The method of any one of claims 1, 2 and 66, wherein said one or more DNA polymerases produce less than about 5% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

70. (Previously presented) The method of any one of claims 1, 2 and 66, wherein said one or more DNA polymerases produce less than about 1% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

71. (Previously presented) The kit of claim 23, wherein said one or more DNA polymerases produce less than about 5% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

72. (Previously presented) The kit of claim 23, wherein said one or more DNA polymerases produce less than about 1% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

73. (Currently amended) The method of any one of claims 1, 2 and 66, wherein less than about 20% of said amplified DNA fragments have one or more non-templated 3′ nucleotides.

74. (Previously presented) The method of any one of claims 1, 2 and 66, wherein less than about 10% of said amplified DNA fragments have one or more non-templated 3′ nucleotides.

75. (Previously presented) The method of any one of claims 1, 2 and 66, wherein less than about 5% of said amplified DNA fragments have one or more non-templated 3′ nucleotides.

76. (Previously presented) The method of any one of claims 1, 2 and 66, wherein less than about 1% of said amplified DNA fragments have one or more non-templated 3′ nucleotides.

77. (Previously presented) The kit of claim 23, wherein less than about 20% of said DNA fragments have one or more non-templated 3′ nucleotides.

78. (Previously presented) The kit of claim 23, wherein less than about 10% of said DNA fragments have one or more non-templated 3′ nucleotides.

79. (Previously presented) The kit of claim 23, wherein less than about 5% of said DNA fragments have one or more non-templated 3′ nucleotides.

80. (Previously presented) The kit of claim 23, wherein less than about 1% of said DNA fragments have one or more non-templated 3′ nucleotides.

81. (Previously presented) The kit of claim 23, wherein said one or more DNA polymerases produce less than about 30% of amplification products containing one or more non-templated nucleotides at their 3′ termini.

82. (Previously presented) The method of any one of claims 1, 2 and 66, wherein said one or more DNA polymerases produce less than about 30% of amplification products containing one or more non-templated nucleotides at their 3′ termini.